

EXPRESS MAIL  
EL360933793US  
ATTY. DKT. 266/187  
SHEET 1 OF 11

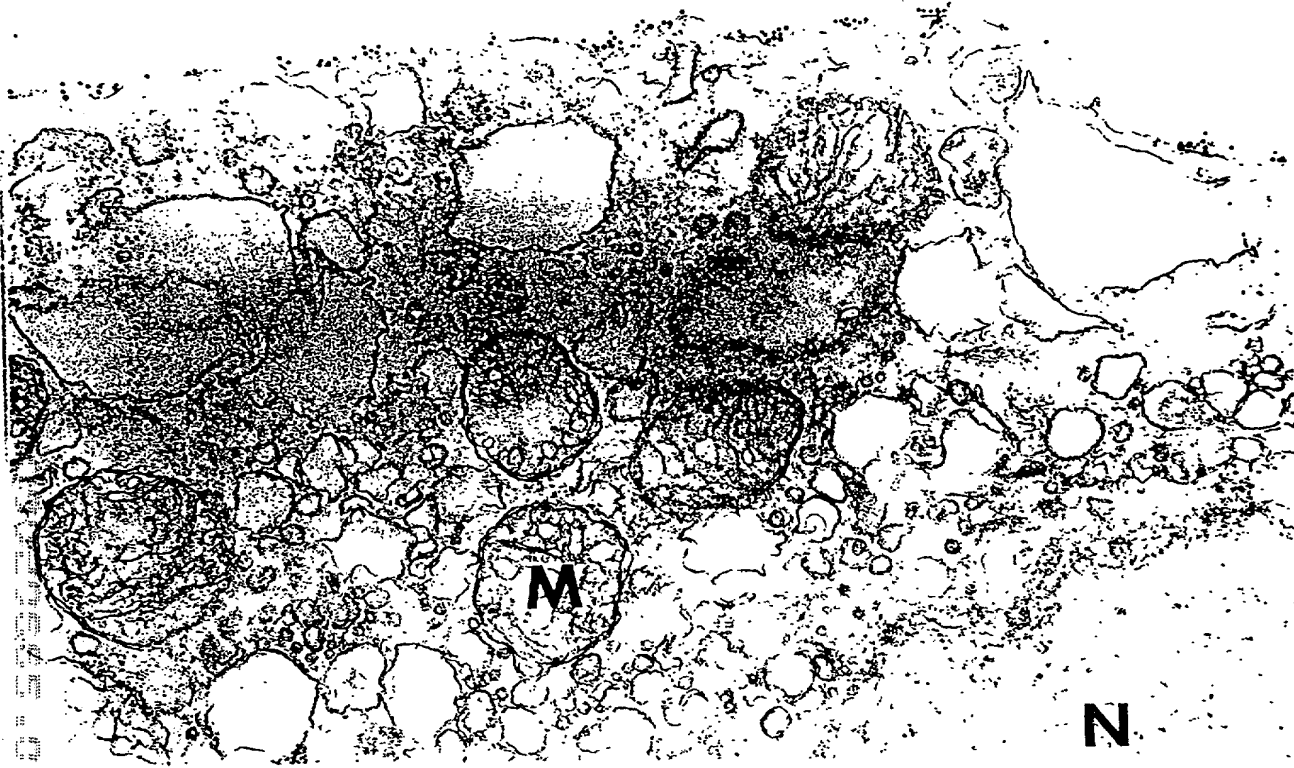


FIGURE 1

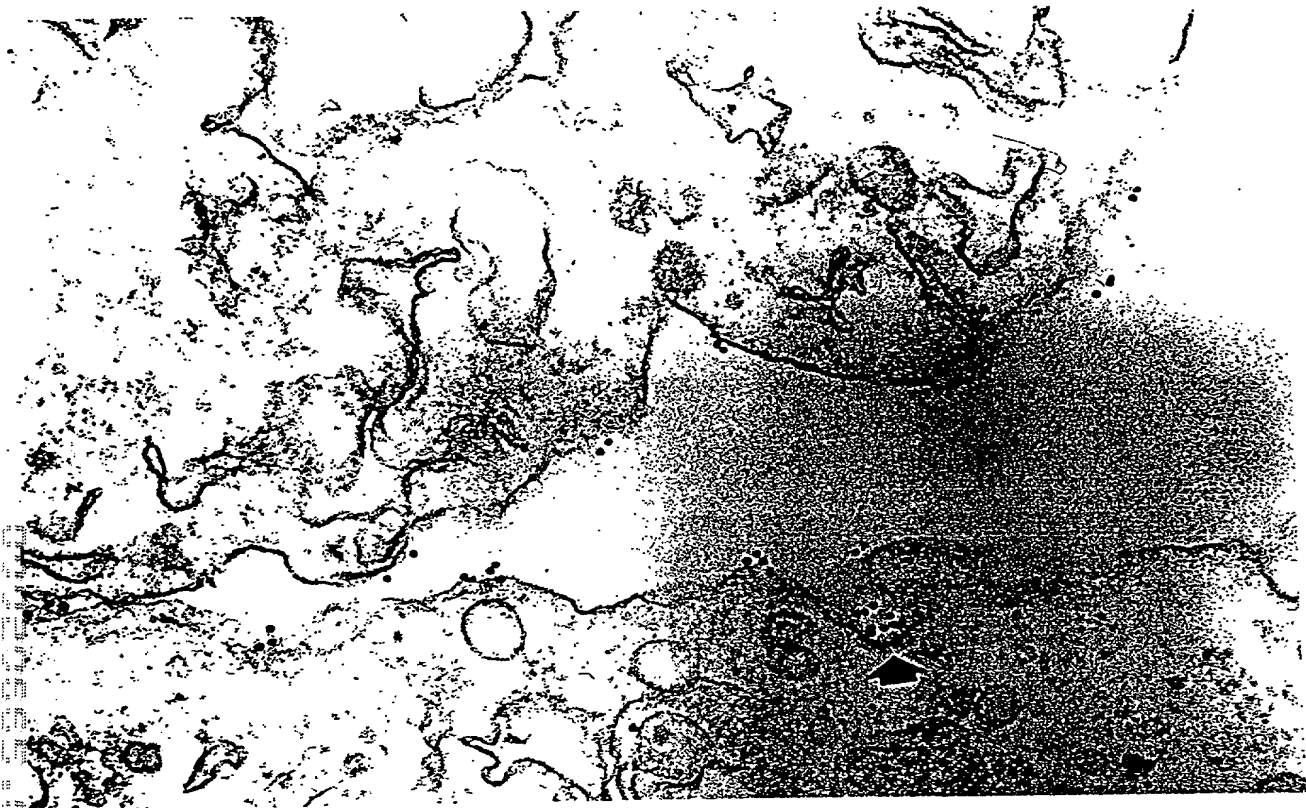


FIGURE 2

EXPRESS MAIL  
EL360933793US  
ATTY. DKT. 266/187  
SHEET 3 OF 11

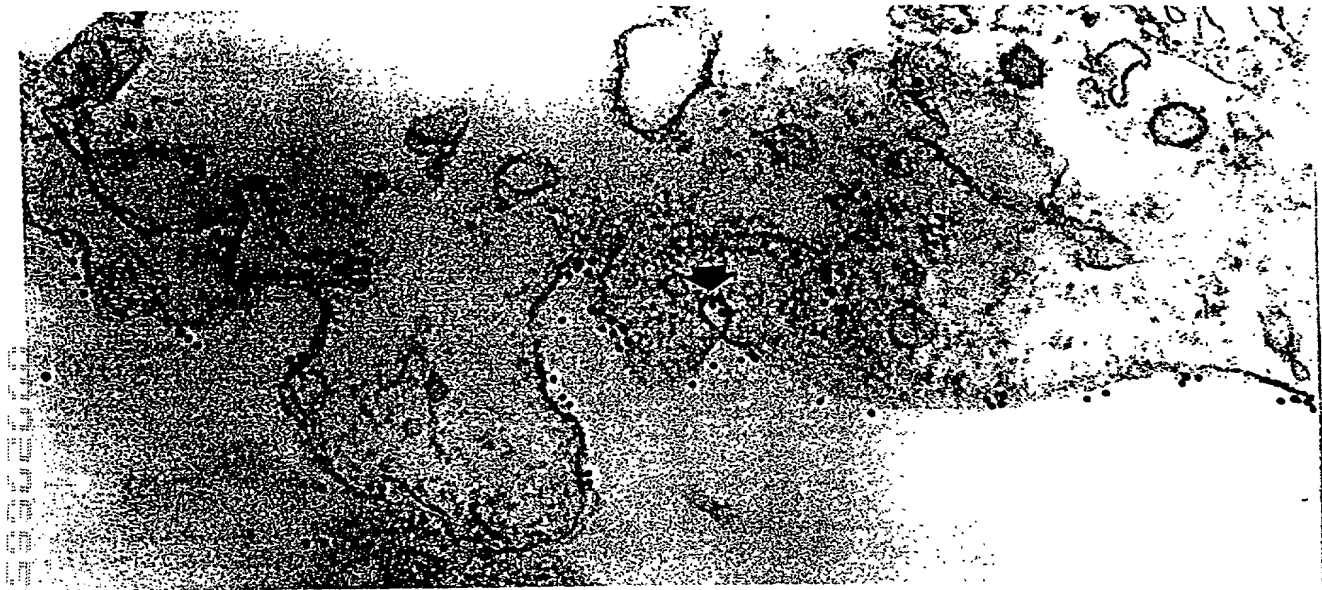


FIGURE 3

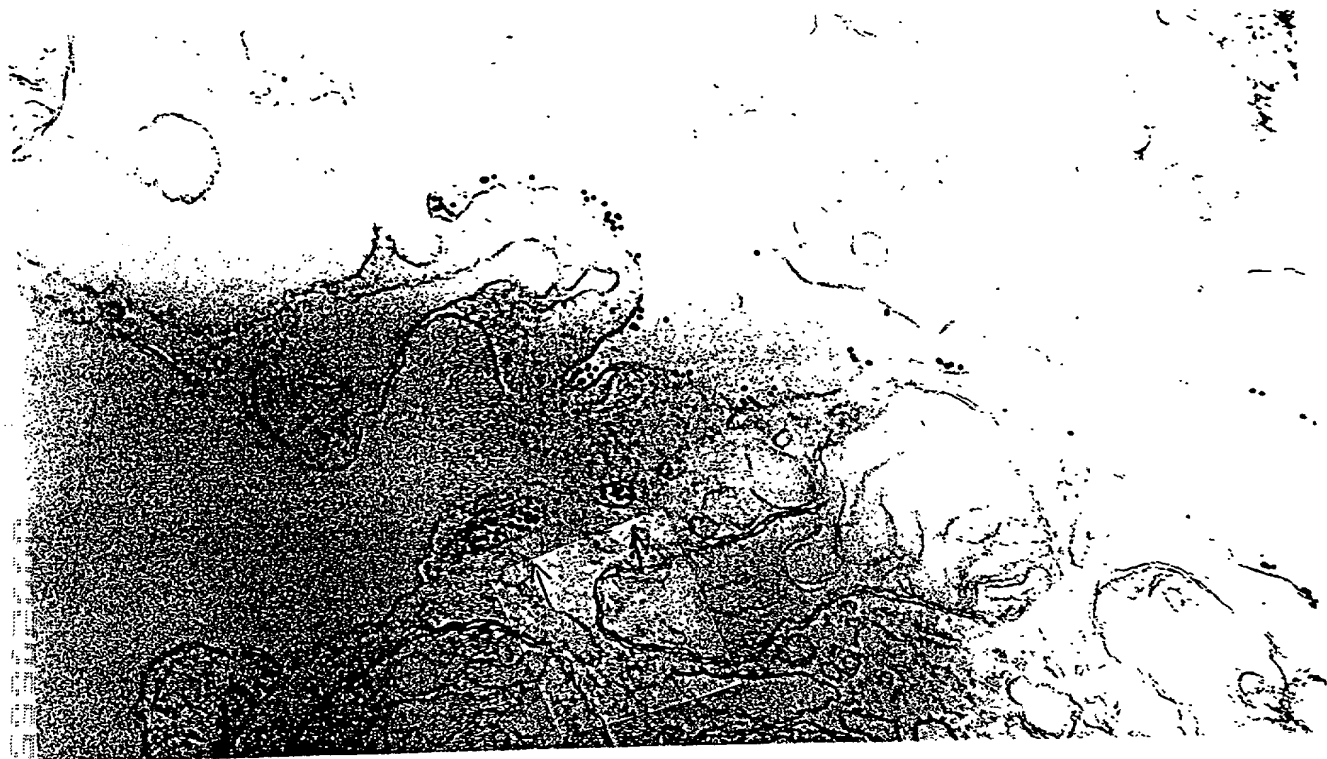


FIGURE 4



FIGURE 5

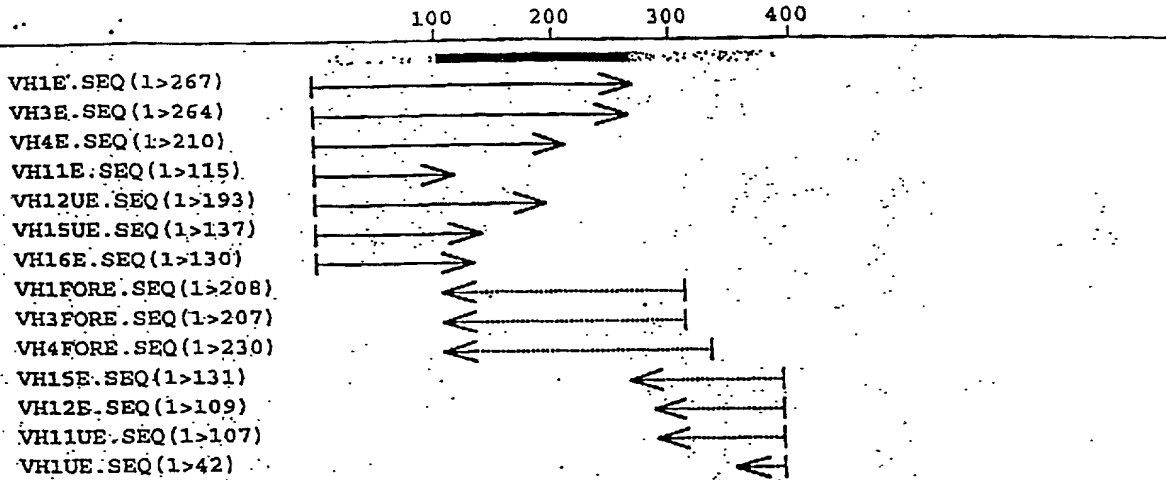


FIGURE 6

Enzymes: All 74 enzymes (No Filter)  
Settings: Linear, Certain Sites Only, Standard Genetic Code

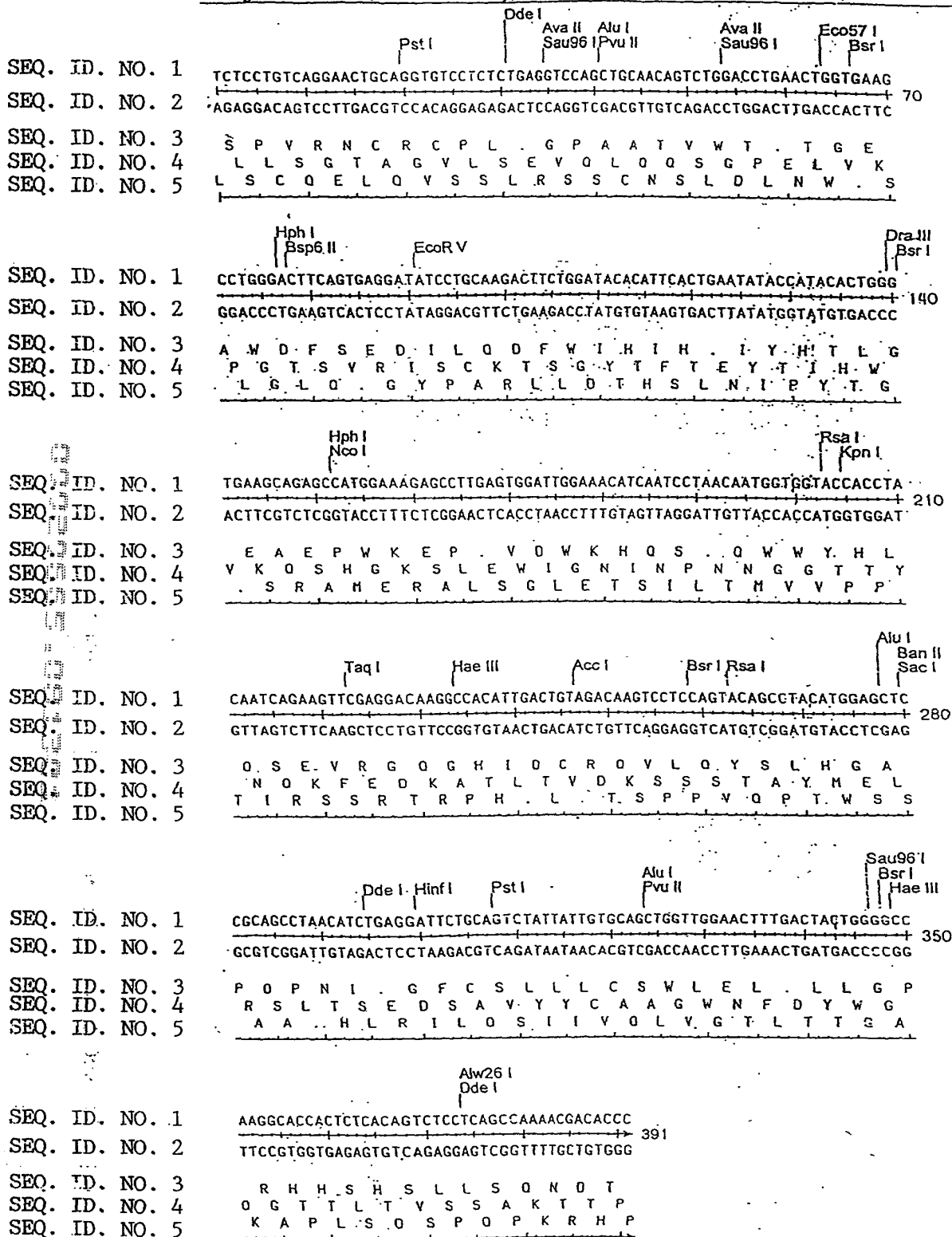


FIGURE 7

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>115)	Seq2(1>125)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VH.PRO	MUVHIIA.PRO				
(1>115)	(1>125)	75.6	2	10	125

```

      10      20      30      40      50
EVQLQQSGPELVKPGTSYRISCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGGTT
EVQLQQSGPELVKPG:SY:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNNWVKOSPGKSLEWIGDINPGNGGTS
      10      20      30      40      50      60
60      70      80      90      100      110
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGQGT
YNQKF:KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G ..FDYWGQGT
YNQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGT
      70      80      90      100      110      120

```

LTVSS  
 :TVSS  
 VTVSS

FIGURE 8



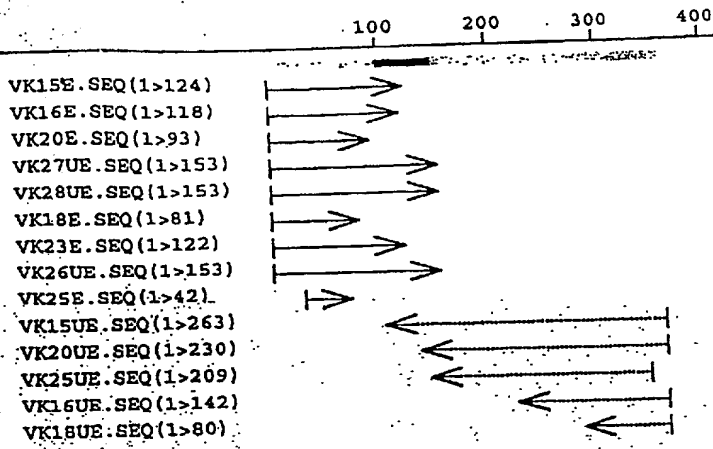


FIGURE 9

Enzymes: All 74 enzymes (No Filter)  
Settings: Linear, Certain Sites Only, Standard Genetic Code

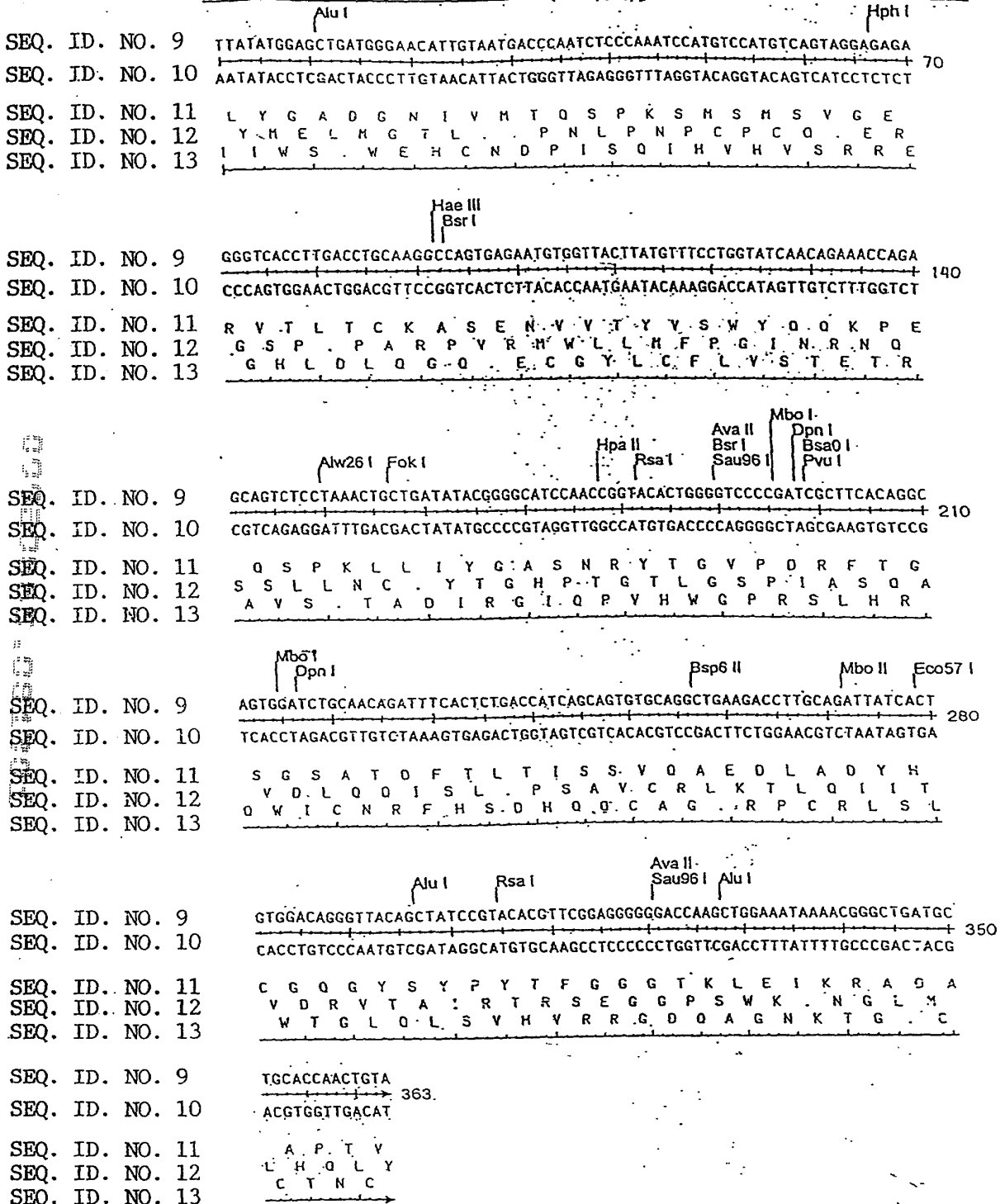


FIGURE 10

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>107)	Seq2(1>111)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VK.PRO	MUVKV.PRO				
(1>107)	(1>109)	60.4	2	2	109

```

      10 20 30 40 50
NIVMTQSPKSMMSVGERVTLTCKAS-ENVVTYVSWYQOKPEQSPKLLIYGASNRYTGVP
: I MTQSP.S:S S:G:RVT:TC:AS ::: Y::WYQOKP. SPKLLIY AS. :GVP
DIOMTQSPSSLSASLGDRVTITCRASQDDISNYLNWYQOKPGGSPKLLIYYASRLHSGVP
      10 20 30 40 50 60
60 70 80 90 100
DRFTGSGSATDFTLTISVVOAEDLADYHCGGYSY-PYTFGGGKLEIK
RE:GSGS:TD::LTIS:::ED:A.Y C QG:: P TFGGKLEIK
SRFSGSGSGTDYSLTISNLEQEDIATYFCQGGNTLPRTFGGKLEIK
      70 80 90 100

```

FIGURE 11